

**BLAST2 Search Results****EXHIBIT A**

Docket No.: PF-0609 USN

USSN: 09/806,267

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Program: blastp**Sequence ID(s):**☐ 1859631CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 1859631CD1
(254 letters)

Database: genpept137
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
<input checked="" type="checkbox"/> <u>g6807669</u> hypothetical protein [Homo sapiens]	520	e-146
<input checked="" type="checkbox"/> <u>g5731207</u> CRIB-containing BORG2 protein [Homo sapiens]	520	e-146
<input checked="" type="checkbox"/> <u>g30585393</u> Homo sapiens CDC42 effector protein (Rho GTPase bin	520	e-146
<input checked="" type="checkbox"/> <u>g30583219</u> CDC42 effector protein (Rho GTPase binding) 3 [Homo	520	e-146
<input checked="" type="checkbox"/> <u>g17939543</u> Unknown (protein for MGC:3481) [Homo sapiens]	520	e-146
<input checked="" type="checkbox"/> <u>g3834633</u> MSE55-related protein [Homo sapiens]	518	e-146
<input checked="" type="checkbox"/> <u>g4324454</u> Cdc42 effector protein 3 [Homo sapiens]	518	e-146
<input checked="" type="checkbox"/> <u>g21961178</u> CDC42 effector protein (Rho GTPase binding) 3 [Mus	483	e-135
<input checked="" type="checkbox"/> <u>g18204088</u> CDC42 effector protein (Rho GTPase binding) 3 [Mus	483	e-135
<input checked="" type="checkbox"/> <u>g12859655</u> unnamed protein product [Mus musculus]	483	e-135

>g6807669 hypothetical protein [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
Query: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L
Sbjct: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240
Query: 241 SLLDEV L N V M D K N K 254
SLLDEV L N V M D K N K
Sbjct: 241 SLLDEV L N V M D K N K 254

>g5731207 CRIB-containing BORG2 protein [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
Query: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L
Sbjct: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQDLGP 240
Query: 241 SLLDEV L N V M D K N K 254
SLLDEV L N V M D K N K
Sbjct: 241 SLLDEV L N V M D K N K 254

>g30585393 Homo sapiens CDC42 effector protein (Rho GTPase binding)
3 [synthetic construct]
Length = 255

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
Query: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L
Sbjct: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNVMMDKNK 254
SLLDEVNLNVMMDKNK
Sbjct: 241 SLLDEVNLNVMMDKNK 254

>g30583219 CDC42 effector protein (Rho GTPase binding) 3 [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEKAAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEKAAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEKAAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNVMMDKNK 254
SLLDEVNLNVMMDKNK
Sbjct: 241 SLLDEVNLNVMMDKNK 254

>g17939543 Unknown (protein for MGC:3481) [Homo sapiens]
Length = 254

Score = 520 bits (1326), Expect = e-146
Identities = 254/254 (100%), Positives = 254/254 (100%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEKAAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEKAAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEKAAHLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVNLNVMMDKNK 254
SLLDEVNLNVMMDKNK
Sbjct: 241 SLLDEVNLNVMMDKNK 254

>g3834633 MSE55-related protein [Homo sapiens]
Length = 254

Score = 518 bits (1320), Expect = e-146
Identities = 253/254 (99%), Positives = 253/254 (99%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEK A HLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEK A HLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEK A HLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLL LQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLFLQLDLGP 240

Query: 241 SLLDEV LNVMDKNK 254
SLLDEV LNVMDKNK
Sbjct: 241 SLLDEV LNVMDKNK 254

>g4324454 Cdc42 effector protein 3 [Homo sapiens]
Length = 254

Score = 518 bits (1319), Expect = e-146
Identities = 253/254 (99%), Positives = 253/254 (99%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGD SFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDNSFLQ 60

Query: 61 GNYELLPGNQEK A HLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120
GNYELLPGNQEK A HLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML
Sbjct: 61 GNYELLPGNQEK A HLGQFPGHNEFFRANSTSDSVFTETPSPVLKNAISLPTIGGSQALML 120

Query: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180
PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ
Sbjct: 121 PLLSPVTFNSKQESFGPAKLPRLSCEPVMEEKAQEKSSLENGTVHQGDTSWGSSGSASQ 180

Query: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240
SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP
Sbjct: 181 SSQGRDSHSSSLSEQYPDWPAEDMFDHPTPCELIKGKTKSEESLSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEV LNVMDKNK 254
SLLDEV LNVMDKNK
Sbjct: 241 SLLDEV LNVMDKNK 254

>g21961178 CDC42 effector protein (Rho GTPase binding) 3 [Mus musculus]
Length = 254

Score = 483 bits (1230), Expect = e-135
Identities = 235/254 (92%), Positives = 242/254 (94%)

Query: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60
MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ
Sbjct: 1 MPAKTPIYLKAANNKKGKKFKLRDILSPDMISPPLGDFRHTIHIGKEGQHDVFGDISFLQ 60

Query: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
GNYELLPGNQEK A H G Q F P G H N + F F R A N S T S D S + F T E T P S P V L K N A I S L P T I G G S Q A L M L
Sbjct: 61 GNYELLPGNQEK A H S G Q F P G H N D F F R A N S T S D S M F T E T P S P V L K N A I S L P T I G G S Q A L M L 120

Query: 121 P L L S P V T F N S K Q E S F G P A K L P R L S C E P V M E E K A Q E K S S L L E N G T V H Q G D T S W G S S G S A S Q 180
P L L S P V T F + S K Q E S F G K L P R L S C E P V M E E K Q E + S S L L E N G V H Q G D T S W G S S G S S Q
Sbjct: 121 P L L S P V T F H S K Q E S F G R P K L P R L S C E P V M E E K V Q E Q S S L L E N G A V H Q G D T S W G S S G S G S Q 180

Query: 181 S S Q G R D S H S S S L S E Q Y P D W P A E D M F D H P T P C E L I K G K T K S E E S L S D L T G S L L S L Q L D L G P 240
S S Q G R D S H S S S L S E Q D W P A + D M F + H P C E L + K K T K S E E S S D L T G S L L S L Q L D L G P
Sbjct: 181 S S Q G R D S H S S S L S E Q S S D W P A D D M F E H P A S C E L V K S K T K S E E S F S D L T G S L L S L Q L D L G P 240

Query: 241 S L L D E V L N V M D K N K 254
S L L D E V L N V M D K N K
Sbjct: 241 S L L D E V L N V M D K N K 254

>g18204088 CDC42 effector protein (Rho GTPase binding) 3 [Mus musculus]
Length = 254

Score = 483 bits (1230), Expect = e-135
Identities = 235/254 (92%), Positives = 242/254 (94%)

Query: 1 M P A K T P I Y L K A A N N K K G K K F K L R D I L S P D M I S P P L G D F R H T I H I G K E G Q H D V F G D I S F L Q 60
M P A K T P I Y L K A A N N K K G K K F K L R D I L S P D M I S P P L G D F R H T I H I G K E G Q H D V F G D I S F L Q
Sbjct: 1 M P A K T P I Y L K A A N N K K G K K F K L R D I L S P D M I S P P L G D F R H T I H I G K E G Q H D V F G D I S F L Q 60

Query: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
GNYELLPGNQEK A H G Q F P G H N + F F R A N S T S D S + F T E T P S P V L K N A I S L P T I G G S Q A L M L
Sbjct: 61 GNYELLPGNQEK A H S G Q F P G H N D F F R A N S T S D S M F T E T P S P V L K N A I S L P T I G G S Q A L M L 120

Query: 121 P L L S P V T F N S K Q E S F G P A K L P R L S C E P V M E E K A Q E K S S L L E N G T V H Q G D T S W G S S G S A S Q 180
P L L S P V T F + S K Q E S F G K L P R L S C E P V M E E K Q E + S S L L E N G V H Q G D T S W G S S G S S Q
Sbjct: 121 P L L S P V T F H S K Q E S F G R P K L P R L S C E P V M E E K V Q E Q S S L L E N G A V H Q G D T S W G S S G S G S Q 180

Query: 181 S S Q G R D S H S S S L S E Q Y P D W P A E D M F D H P T P C E L I K G K T K S E E S L S D L T G S L L S L Q L D L G P 240
S S Q G R D S H S S S L S E Q D W P A + D M F + H P C E L + K K T K S E E S S D L T G S L L S L Q L D L G P
Sbjct: 181 S S Q G R D S H S S S L S E Q S S D W P A D D M F E H P A S C E L V K S K T K S E E S F S D L T G S L L S L Q L D L G P 240

Query: 241 S L L D E V L N V M D K N K 254
S L L D E V L N V M D K N K
Sbjct: 241 S L L D E V L N V M D K N K 254

>g12859655 unnamed protein product [Mus musculus]
Length = 254

Score = 483 bits (1230), Expect = e-135
Identities = 235/254 (92%), Positives = 242/254 (94%)

Query: 1 M P A K T P I Y L K A A N N K K G K K F K L R D I L S P D M I S P P L G D F R H T I H I G K E G Q H D V F G D I S F L Q 60
M P A K T P I Y L K A A N N K K G K K F K L R D I L S P D M I S P P L G D F R H T I H I G K E G Q H D V F G D I S F L Q
Sbjct: 1 M P A K T P I Y L K A A N N K K G K K F K L R D I L S P D M I S P P L G D F R H T I H I G K E G Q H D V F G D I S F L Q 60

Query: 61 GNYELLPGNQEK A H L G Q F P G H N E F F R A N S T S D S V F T E T P S P V L K N A I S L P T I G G S Q A L M L 120
GNYELLPGNQEK A H G Q F P G H N + F F R A N S T S D S + F T E T P S P V L K N A I S L P T I G G S Q A L M L
Sbjct: 61 GNYELLPGNQEK A H S G Q F P G H N D F F R A N S T S D S M F T E T P S P V L K N A I S L P T I G G S Q A L M L 120

Query: 121 P L L S P V T F N S K Q E S F G P A K L P R L S C E P V M E E K A Q E K S S L L E N G T V H Q G D T S W G S S G S A S Q 180
P L L S P V T F + S K Q E S F G K L P R L S C E P V M E E K Q E + S S L L E N G V H Q G D T S W G S S G S S Q
Sbjct: 121 P L L S P V T F H S K Q E S F G R P K L P R L S C E P V M E E K V Q E Q S S L L E N G A V H Q G D T S W G S S G S G S Q 180

Query: 181 S S Q G R D S H S S S L S E Q Y P D W P A E D M F D H P T P C E L I K G K T K S E E S L S D L T G S L L S L Q L D L G P 240
S S Q G R D S H S S S L S E Q D W P A + D M F + H P C E L + K K T K S E E S S D L T G S L L S L Q L D L G P
Sbjct: 181 S S Q G R D S H S S S L S E Q S S D W P A D D M F E H P A S C E L V K S K T K S E E S F S D L T G S L L S L Q L D L G P 240

Sbjct: 181 SSQGRDSHSSSLSEQSSDWPADDMFEHPASCELVKSKTKSEESFSDLTGSLLSLQLDLGP 240

Query: 241 SLLDEVLVNMDKNK 254
SLLDEVLVNMDKNK

Sbjct: 241 SLLDEVLVNMDKNK 254

Database: genpept137

Posted date: Sep 11, 2003 11:22 AM

Number of letters in database: 474,463,515

Number of sequences in database: 1,534,369

Lambda	K	H
0.311	0.131	0.377

Gapped

Lambda	K	H
0.270	0.0470	0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 250360315

Number of Sequences: 1534369

Number of extensions: 10716561

Number of successful extensions: 21567

Number of sequences better than 10.0: 99

Number of HSP's better than 10.0 without gapping: 53

Number of HSP's successfully gapped in prelim test: 46

Number of HSP's that attempted gapping in prelim test: 21369

Number of HSP's gapped (non-prelim): 184

length of query: 254

length of database: 474,463,515

effective HSP length: 60

effective length of query: 194

effective length of database: 382,401,375

effective search space: 74185866750

effective search space used: 74185866750

T: 11

A: 40

X1: 16 (7.2 bits)

X2: 38 (14.8 bits)

X3: 64 (24.9 bits)

S1: 42 (21.8 bits)

Graphical Viewer...

Submit sequences to:

